

Patent Claims

1. Use of polypeptides with the biological activity of a very long chain fatty acid elongase for identifying herbicidally active compounds
2. Use according to Claim 1, characterized in that the polypeptides are 60% homologous with the polypeptide according to SEQ ID NO: 2.
3. Use according to Claim 1, characterized in that the herbicidally active compounds are modulators of these polypeptides.
4. Use according to any one of Claims 1 to 3, characterized in that the polypeptides include a sequence which is selected from
 - a) the sequence shown in SEQ ID NO: 2,
 - b) sequences encoded by a nucleic acid having SEQ ID NO: 1,
 - c) partial sequences of the sequences defined under a) or b) which still have the biological activity of a VLCFAE,
 - d) sequences which have an identity of at least 60%, preferably of 80%, particularly preferably of 90%, with the sequences defined under a) to c),
 - e) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,
 - f) sequences which have an identity of at least 60%, preferably of 80%, particularly preferably of 90%, with the sequences defined under e),

g) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

h) sequences which have an identity of at least 60%, preferably of 80%, particularly preferably of 90%, with the sequences defined under g).

5. Use of nucleic acids which code for polypeptides with the biological activity of a very long chain fatty acid elongase in methods for identifying modulators of these polypeptides.

6. Use of nucleic acids which code for polypeptides with the biological activity of a very long chain fatty acid elongase for identifying substances which alter the expression of the polypeptides encoded by them.

7. Use according to Claim 5 or 6, characterized in that single-stranded or double-stranded DNA or RNA is involved.

8. Use according to Claim 5 or 6, characterized in that fragments of genomic DNA or cDNA are involved.

9. Use according to any of Claims 5 to 8, characterized in that the nucleic acids comprise a sequence which is selected from

a) the sequence shown in SEQ ID NO: 1,

b) sequences which code for a polypeptide including the amino acid sequence shown in SEQ ID NO: 2,

c) partial sequences at least 14 base-pairs long of the sequences defined under a) or b),

- d) sequences which hybridize to the sequences defined under a) or b),
- e) sequences which have an identity of at least 60%, preferably of 80%, particularly preferably of 90%, with the sequences defined under a) or b),
- f) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2
- g) sequences which have an identity of at least 60%, preferably of 80%, particularly preferably of 90%, with the sequences defined under f),
- h) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,
- i) sequences which have an identity of at least 60%, preferably of 80%, particularly preferably of 90%, with the sequences defined under h),
- j) sequences which are complementary to the sequences defined under a) to i), and
- k) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to h).

- 10. Use of a DNA construct comprising a nucleic acid having SEQ ID NO: 1 and of a heterologous promoter in methods for identifying herbicidally active compounds.
- 11. Use of a vector comprising a nucleic acid having SEQ ID NO:1, in methods for identifying herbicidally active compounds.

12. Use of a host cell containing a nucleic acid coding for a polypeptide having SEQ ID NO: 2 in methods for identifying herbicidally active compounds.
13. Use according to Claim 12, characterized in that the host cell used is *E. coli*.
14. Use of a host cell according to claim 13, characterized in that a yeast, insect, mammalian or plant cell is involved.
15. Method for finding a chemical compound which binds to a polypeptide with the biological activity of a very long chain fatty acid elongase, comprising the following steps:
 - a) contacting a polypeptide with the biological activity of a very long chain fatty acid elongase or a host cell containing a polypeptide with a chemical compound or a mixture of chemical compounds under conditions which permit the interaction of a chemical compound with the polypeptide, and
 - b) determining the chemical compound which specifically binds to the polypeptide.
16. Method for finding inhibitors and/or activators of a polypeptide with the biological activity of a very long chain fatty acid elongase, comprising the following steps:
 - a) contacting a polypeptide with the biological activity of a very long chain fatty acid elongase or a host cell containing a polypeptide with a chemical compound or a mixture of chemical compounds under conditions which permit the interaction of a chemical compound with the polypeptide, and

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- 5 21. Herbicidally active substances which are found by a method according to Claims 16 or 17.
22. Use of the nucleic acid coding for a polypeptide having SEQ ID NO: 2 for producing transgenic plants.
- 10 23. Transgenic plants, parts of plants, protoplasts, plant tissues or plant propagation materials, characterized in that, after introduction of a nucleic acid coding for a polypeptide having SEQ ID NO: 2, the intracellular concentration of a polypeptide according to Claim 14 is increased or reduced compared with the corresponding wild-type cells.
- 15 24. Plants, parts of plants, protoplasts, plant tissues or plant propagation materials, characterized in that they contain a polypeptide having SEQ ID NO: 2 whose biological activity or expression pattern is altered by comparison with the corresponding endogenous polypeptides.

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